```
CLUSTAL 2.0.12 multiple sequence alignment


SIN2     ------------------------------------------------------------
SIN4     MRGGASSGPQRWGSAGTTPRSLSTGSSPRGSDD--RSSDDGEELVEVTLDLQDDDTIVLR 58
SIN6     MRGLPGHERR-WTSDTVSSDKDFSGELSPGADSGYNSGFASEEFVEVTLDLQDDDTIILR 59
SIN8     MRGLPGHERR-WTSDTVSSGKDLSGESSPGTDSGNISGFASEEFVEVILDLQDDDTIILR 59
SIN10    MRGLPGHERR-WTSDTVSSGKDLSGESSPGTDSGNISGFASEEFVEVILDLQDDDTIILR 59
SIN12    MKPFSKNDRRRWSFDSVSAGKTAVGSASTSPGT-EYSINGDQEFVEVTIDLQDDDTIVLR 59
SIN14    ----------MKMRRGNSSNDHELGILRGANSDTNSDTESIASDRGAFSGPLGRP--KR 47
SIN16    ------------MQ--NSENHHPH------HQHHHSDTEIIGNDRASYSGPLSGPLNKR 39
SIN18    ------------------------------------------------------------
SIN20    ------------------MSRVSFEVS------GGYHSDAEAGNS--GPMSGGQLPPIYKK 35
SIN22    ------------------------------MMNRSEMQKLGFEHVRYYT--ESPYNRG 26


SIN2     ------------------------------------------------------------
SIN4     SVEPAAAAAAG-----VGAGAGAASARGELTGGPSSSSSRSRSPSIRRSS-SHRLLQFSQ 112
SIN6     SVEPATVINIDAPDLPAGVGISGVSIE---TPTSAS-VSESRSPTIRRSS-SSKLRQFSQ 114
SIN8     SVEPATVINIDASDPATGVGIGGVSIE---TPASLTSTSGTRSPTMRRST-SNKLRQFSQ 115
SIN10    SVEPATVINIDGSDPASGVGIGGASIE---TPASVTSTSETRSPMMRRST-SNKFRQFSQ 115
SIN12    SVEPATAINV---------IGDISDD---NTGIMTPVSISRSPTMKRTS-SNRFRQFSQ 105
SIN14    ASKKNARF--ADDLPKRSNSVAGGRGD---DDEYVEITLDIRDDSVAVHS-VQQAAGGGG 101
SIN16    GGKKSARFNIPESTDIGTSVGTGGKSN---DDAYVEITLDVREDSVAVHS-VKTAGG--D 93
SIN18    -------------------------------MASPYDHQSPHAQHPSGLPRPPGAGA 26
SIN20    PG--NSRF---------TAENSQRTR---TAPYVDLTVDVQDDTVSVHS-LKMEGGS-S 78
SIN22    ESSANVAT-----------TSNYYGE---DEPYVEITLDIHDDSVSVYG-LKSPNHRGA 70


SIN2     ------------------------------------------------------------
SIN4     ELKAEAMARARQFSQDLT---KRFGRSH--------------SRSEAQAPSG-LESAL--A 153
SIN6     ELKAEAVAKARQFSQELKAELRRFSWSHGHASRAFSPSSFFQNAVVGTGNG-VDSAL--A 171
SIN8     ELKAEAVAKAKHFSQELKAELRRFSWSHGHASRTFSPASFFQNAVVGTGNG-VDSAL--A 172
SIN10    ELKAEAVAKAKHFSQELKAELRRFSWSHGHASRAFSPASFFQNAVVGTGNG-VDSAL--A 172
SIN12    ELKAEAVAKAKQLSQELK----RFSWSRSFSG-NLTTTSTAANQSGGAGGGLVNSAL--E 158
SIN14    HLEDPELALLTKKTLESSLNNTTSLSFFRS-----------TSSRIKNASRELRRVF--S 148
SIN16    DVEDPELALLAKG-LEK--KSTLGSSLVRN-----------ASSRIRQVSQELRRLA--S 137
SIN18    GAAAGGFARGLMKQPSR-----------------------LASGVRQFASRVSMKVPEG 62
SIN20    VEESPELTLLKRNRLEK---KTTVVKRLAS----------VSHELKRLTSVSGGIG--G 122
SIN22    GSNYEDQSLLRQGRSGR--SNSVLKRLASS----------VSTGITRVASSVSSSS--A 115


SIN2     ------------------------------------------------------------
SIN4     ARAARRQRAQLDRTRSGAHKALRGLRFISSNKA-NNAWMEVQANFDRLAR--DGYLSRSD 210
SIN6     ARALRRQRAQLDRTRSSAHRALRRLKFISNNK--TNGWNEVENNFSKLAK--DGYLYRSD 227
SIN8     ARALRRQRAQLDRTRSSAHKALRGLKFISNNK--TNGWNEVENNFAKLAK--DGYLYRSD 228
SIN10    ARALRRQRAQLDRTRSSAHKALRGLKFISNNK--TNGWNEVENNFAKLAK--DGYLYRSD 228
SIN12    ARALRKQRAQLDRTRSSAQRALRGLRFISNKQKNVDGWNDVQSNFEKFEK--NGYIYRSD 216
SIN14    RRPSPAVR-RFDRTSSAAIHALKGLKFIATKT---AAWPAVDQRFDKLSADSNGLLLSAK 204
SIN16    LNKRPIPTGRFDRNKSAAAHALKGLKFISKTDG-GAGWAAVEKRFDEITASTTGLLPRAK 196
SIN18    VGGMRPGGGRMTRMQSSAQVGLRGLRFLDKTSGGKEGWKSVERRFDEMNR--NGRLPKES 120
SIN20    RK--PPRPAKLDRTKSAASQALKGLKFISKTDG-GAGWSAVEKRFNQITATTGGLLLRTK 179
SIN22    RKPPRPQLAKLRRSKSRAELALKGLKFITKTDG-VTGWPEVEKRFYVMTMTNNGLLHRSR 174
                                    SEQ ID NO:25


SIN2     ------------------------------------------------------------
SIN4     FAECIG--------------------------MTESKEFALELFDTLSRRRQMK-VDTIN 243
SIN6     FAQCIG--------------------------MKDSKEFALELFDALSRRRRLK-VDKIS 260
SIN8     FAQCIG--------------------------MKDSKEFALELFDALSRRRRLK-VDKIS 261
SIN10    FAQCIGQYSRRRSLQFNYRLITLILINYLVKGMKDSKEFALELFDALSRRRRLK-VDKIS 287
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SIN12   FAQCIG------------------------MKDSKEFALELFDALSRRRRLK-VEKIN 249
SIN14   FWECLG------------------------MNKESKDFADQLFRALARRNNVS-GDAIT 238
SIN16   FGECIG------------------------MNKESKEFAVELYDALARRRNIT-TDSIN 230
SIN18   FGKCIG------------------------MGDSKEFAGELFVALARRRNLEPEDGIT 154
SIN20   FGECIG------------------------MT--SKDFALELFDALARRRNIT-GEVID 211
SIN22   FGECIG------------------------MK--STEFALALFDALARRENVS-GDSIN 206


SIN2    ------------------------------------------------------------
SIN4    KDELREIWQQITDNSFDSRLQIFFEMVDKNADGRITEAEVKEIIMLSASANKLSRLKEQA 303
SIN6    KEELYEYWSQITDQSFDSRLQISFDMVDKNEDGRIAEEEVKEIIMLSASANKLSRLKEQA 320
SIN8    KEELYEYWSQITDQSFDSRLQIFFDMVDKNEDGRIGEEEVKEIIMLSASANKLSRLKEQA 321
SIN10   QEELYEYWSQITDQSFDSRLQIFFDMVDKNEDGRIGEEEVKEIIMLSASANKLSRLKEQA 347
SIN12   HDELYEYWSQINDESFDSRLQIFFDIVDKNEDGRITEEEVKEIIMLSASANKLSRLKEQA 309
SIN14   KEQLRIFWEQISDESFDAKLQVFFDMVDKDEDGRVTEEEVAEIISLSASANKLSNIQKQA 298
SIN16   KAQLKEFWDQVADQSFDSRLQTFFDMVDKDADGRITEEEVREIIGLSASANRLSTIQKQA 290
SIN18   KEQLKEFWEEMTDQNFDSRLRIFFDMCDKNGDGMLTEDEVKEVIILSASANKLAKLKGHA 214
SIN20   GDQLKEFWEQINDQSFDSRLKTFFDMVDKDADGRLTEDEVREL---------------- 254
SIN22   MNELKEFWKQITDQDFDSRLRTFFAMVDKDSDGRLNEAEVREIITLSASANELDNIRRQA 266
                                        SEQ ID NO:26      SEQ ID NO:27

SIN2    ------------------------------------------------------------
SIN4    EEYAALIMEELDPEGLGYIELWQLETLLLQK--DTYMNYSQALSYTSQALSQNLAGLRKK 361
SIN6    EEYAALIMEELDPERLGYIELWQLETLLLQK--DTYLNYSQALSYTSQALSQNLHGLRKK 378
SIN8    EEYAALIMEELDPERLGYIELWQLETLLLQK--DTYLNYSQALSYTSQALSQNLQGLRKR 379
SIN10   EEYAALIMEELDPERLGYIELWQLETLLLQK--DTYLNYSQALSYTSQALSQNLQGLRKR 405
SIN12   EEYAALIMEELDPERLGYIELWQLETLLLQK--DTYLNYSQALSYTSQALSQNLQGLRGK 367
SIN14   KEYAALIMEELDPDNAGFIMIENLEMLLLQAPNQSVRMG--DSRILSQMLSQKLRPAKES 356
SIN16   DEYAAMIMEELDPNNLGYIMIENLEMLLLQAPNQSVQRGG-ESRNLSQMLSQKLKHTQER 349
SIN18   ATYASLIMEELDPDDRGYIEIWQLETLLRGM--VSAQAAPEKMKRTTSSLARTMIPSRYR 272
SIN20   --------------------ESLETLLLQAATQSVITSTGERKNLSHMMSQRLKPTFNR 293
SIN22   DEYAALIMEELDPYHYGYIMIENLEILLLQAPMQDVRDG--ESKKLSKMLSQNLMVPQSR 324
             SEQ ID NO:28

SIN2    ------------------------------------------------------------
SIN4    SSIRKISTSLSYYFEDNWKRLWVLALWIGIMAGLFTWKFMQYRNRYVFDVMGYCVTTAKG 421
SIN6    SPIKRMSTKLVYSLQENWKRIWVLTLWILIMIGLFLWKFYQKNKSAFRVMGYCLVTAKG 438
SIN8    SPIRRMSTKLVYSLQENWKRIWVLVLWILIMIGLFLWKFYLYKQKSAFQVMGYCLLTAKG 439
SIN10   SPIRRMSTKLVYSLQENWKRIWVLVLWILIMIGLFLWKFYQYKQKSAFQVMGYCLLTAKG 465
SIN12   SRIHRMSSDFVYIMQENWKRIWVLSLWIMIMIGLFLWKFFQYKQKDAFHVMGYCLLTAKG 427
SIN14   NPLLRWSEKIKYFILDNWQRLWIMMLWLGICGGLFTYKFIQYKNKAAYGVMGYCVCVAKG 416
SIN16   NPIVRWYKSFMYFLLDNWQRVWVLLLWIGIMAGLFTWKYIQYKEKAAYKVMGPCVCFAKG 409
SIN18   SPLKRHVSRTVDFVHENWKRIWLVALWLAVNVGLFAYKFEQYERRAAFQVMGHCVCVAKG 332
SIN20   NPLKRWYRGLRFFLLDNWQRCWVIVLWFIVMAILFTYKYIQYRRSPVYPVMGDCVCMAKG 353
SIN22   NLGARFCRGMKYFLFDNWKRVWVMALWIGAMAGLFTWKFMEYRKRSAYEVMGVCVCIAKG 384


SIN2    ------------------------------------------------------------
SIN4    AAETLKLNMAIILLPVCRNTITWLR-STRAARALPFDDNINFHKTIAAAIVVGIILHAGN 480
SIN6    AAETLKFNMALILLPVCRNTITWLR-STKLSHFVPFDDNINFHKTVAAAIVTGIILHAGN 497
SIN8    AAETLKFNMALILLPVCRNTITFLR-STKLSCFVPFDDNINFHKTVAAAIVTGIILHAGN 498
SIN10   AAETLKFNMALILLPVCRNTITFLR-STKLSCFVPFDDNINFHKTVAAAIVTGIILHAGN 524
SIN12   AAETLKFNMALILFPVCRNTITWLR-STRLSYFVPFDDNINFHKTIAGAIVVAVILHIGD 486
SIN14   GAETLKFNMALILLPVCRNTITWLRNKTKLGTVVPFDDSLNFHKVIASGIVVGVLLHAGA 476
SIN16   AAETLKLNMAIILFPVCRNTITWLRNKTRLGAAVPFDDNLNFHKVIAVAIALGVGIHGLS 469
SIN18   AAEVLKLNMALILLPVCRNTLTTLR-STALSHVIPFDDNINFHKVIAATIAAATAVHTLA 391
SIN20   AAETVKLNMALILLPVCRNTITWLRNKTRLGRVVPFDDNLNFHKVIAVGIIVGVTMHAGA 413
SIN22   AAETLKLNMAMILLPVCRNTITWLRTKTKLSAIVPFDDSLNFHKVIAIGISVGVGIHATS 444
              SEQ ID NO:29
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SIN2    ------------------------------------------------------------
SIN4    HLVCDFPRLIKSSDEKYAP-LGQYFGE-IKPTYFTLVKGVEGITGVIMVVCMIIAFTLAT 538
SIN6    HLVCDFPRLIHADDQDYQSFLSNDFGQ-SKPGYIDLVKGVEGVTGIIMVILMAIAFTLAT 556
SIN8    HLVCDFPKLIHANNTNYQKYLVNDFGP-SQPQYIDLVKGVEGVTGIIMVILMAIAFTLAT 557
SIN10   HLVCDFPKLIHANSTNYQKYLVNDFGP-SQPQYIDLVKGVEGVTGIVMVILMAIAFTLAT 583
SIN12   HLACDFPRIVRATEYDYNRYLFHYFQT-KQPTYFDLVKGPEGITGILMVILMIISFTLAT 545
SIN14   HLTCDFPRLIAADEDTYEP-MEKYFGD-QPTSYWWFVKGVEGWTGIVMVVLMAIAFTLAT 534
SIN16   HLTCDFPRLLNASEEEYEP-MKYYFGD-QPESYWWFIKGVEGVTGIIMVVLMAIAFTLAT 527
SIN18   HVTCDFPRLINCPSDKFMATLGPNFGY-RQPTYADLLESAPGVTGILMIIIMSFSFTLAT 450
SIN20   HLACDFPRLLHATPEAYRP-LRQFFGDEQPKSYWHFVNSVEGITGLVMVLLMAIAFTLAT 472
SIN22   HLACDFPRLIAADEDQYEP-MEKYFGP-QTKRYLDFVQSVEGVTGIGMVVLMTIAFTLAT 502


SIN2    ------------------------------------------------------------
SIN4    RWFRRSLVK-LPRPFDKLTGFNAFWYSHHLFIIVYIALIVHGECLYLIHV-WYRRTTW-M 595
SIN6    RWFRRSLIK-LPKPFDRLTGFNAFWYSHHLLVIVYILLIIHGTFLFLVHK-WYSKTTW-M 613
SIN8    RWFRRSLIK-FPKPFDRLTGFNAFWYSHHLLIIVYIVLIIHGTFLYLVHN-WYSKTTW-M 614
SIN10   RWFRRSLIK-LPKPFDRLTGFNAFWYSHHLLIIVYIVLIIHGTFLYLVHN-WYSKTTW-M 640
SIN12   RWFRRNLVK-LPKPFDRLTGFNAFWYSHHLFVIVYILLILHGIFLYFAKP-WYVRTTW-M 602
SIN14   PWFRRNKLN-LPNFLKKLTGFNAFWYTHHLFIIVYALLIVHGIKLYLTKI-WYQKTTW-M 591
SIN16   PWFRRNRVS-LPKPFHKLTGXNAFWYSHHLFVIVYTLFIVHGEKLYITKD-WYKRTDMDV 585
SIN18   HSFRRSVVK-LPSPLHHLAGFNAFWYAHHLLVLAYVLLVVHSYFIFLTRE-WYKKTTW-M 507
SIN20   PWFRRGKLNYLPGPLKKLASFNAFWYTHHLFVIVYILLVAHGYYLYLTRD-WHNKTTW-M 530
SIN22   TWFRRNKLN-LPGPLKKITGFNAFWYSHHLFVIVYSLLVVHGFYVYLIIEPWYKKTTW-M 560


SIN2    ------------------------------------------------------------
SIN4    YLSVPVCLYVGERILRFFRSGSYSVRLLKVAIYPGNVLTLQMSKPPTFRYKSGQYMFVQC 655
SIN6    YLAVPVLLYAGERTLRFFRSGLYTVRLLKVAIYPGNVLTLQMSKPPQFRYKSGQYMFVQC 673
SIN8    YLAVPVLLYAGERTLRFFRSGLYTVRLLKVAIYPGNVLTLQMSKPPQFRYKSGQYMFVQC 674
SIN10   YIAVPVLLYAGERTLRFFRSGLYSVRLLKVAIYPGNVLTLQMSKPPQFRYKSGQYMFVQC 700
SIN12   YLAVPVLLYGGERTLRYFRSGSYSVRLLKVAIYPGNVLTLQMSKPTQFRYKSGQYMFVQC 662
SIN14   YLAVPILLYASERLLRAFRSSIKPVKMIKVAVYPGNVLSLHMTKPQGFKYKSGQFMLVNC 651
SIN16   LLTIPIILYASERLIRAFRSSIKAVKILKVAVYPGNVLALHMSKPQGYKYKSGQYMFVNC 645
SIN18   YLIVPVLFYACERTIRKVRENNYRVSIVKAAIYPGNVLSLHMKKPPGFKYKSGMYLFVKC 567
SIN20   YLVVPVVLYACERLIRAFRSSIKAVTIRKVAVYPGNVLAIHLSRPQNFKYKSGQYMFVNC 590
SIN22   YLMVPVVLYLCERLIRAFRSSVEAVSVLKVAVLPGNVLSLHLSRPSNFRYKSGQYMYLNC 620


SIN2    ------------------------------------------------------------
SIN4    PAVSPFEWHPFSITSAPGDDYLSIHVRQLGDWTRELKRVFAAACEPPAGGKSG-LLRAD- 713
SIN6    PAVSPFEWHPFSITSAPGDDYLSIHIRQLGDWTQELKRVFSEACERPEAGKSG-LLRAD- 731
SIN8    PAVSPFEWHPFSITSAPGDDYLSIHIRQLGDWTQELKRVFSEACEQPEAGKSG-LLRAD- 732
SIN10   PAVSPFEWHPFSITSAPGDDYLSIHIRQLGDWTQELKRVFSEACEQPEAGKSG-LLRAD- 758
SIN12   PAVSPFEWHPFSITSAPEDDYISIHIRQLGDWTQELKRVFSEVCEPPVGGKSG-LLRAD- 720
SIN14   RAVSPFEWHPFSITSAPGDDYLSVHIRTLGDWTRKLRTVFSEVCKPPTAGKSG-LLRAD- 709
SIN16   AAVSPFEWHPFSITSAPGDDYLSVHIRTLGDWTRQLKTVFSEVCQPPPNGKSG-LLRADY 704
SIN18   PDVSPFEWHPFSITSAPGDDYLSVHIRTLGDWTTELRNLFGKACEAQVTSKKATLSRLET 627
SIN20   AAVSPFEWHPFSITSAPQDDYLSVHIRVLGDWTRALKGVFSEVCKPPPAGVSG-LLRADM 649
SIN22   SAVSTLEWHPFSITSAPGDDYLSVHIRVLGDWTKQLRSLFSEVCKPRPPDEHR-LNRADS 679
                     SEQ ID NO: 30      SEQ ID NO: 31


SIN2    ------------------------------------------------------------
SIN4    ------ETTKKILPKLLIDGPYGSPAQDYSKYDVLLLVGLGIGATPFISILKDLLNNIIK 767
SIN6    ------ENTKKSLPKLLIDGPYGAPAQDYRKYDVLLLVGLGIGATPFISILKDLLVNIVK 785
SIN8    ------ENTKTSLPKLLIDGPYGAPAQDYRKYDVLLLVGLGIGATPFISILKDLLKNIVT 786
SIN10   ------ENTKTSLPKLLIDGPYGAPAQDYRKYDVLLLVGLGIGATPFISILKDLLKNIVA 812
SIN12   ------ETTKKSLPKLLIDGPYGAPAQDYRKYDVLLLVGLGIGATPFISILKDLLNNIVK 774
SIN14   -----GGDGNLPFPKVLIDGPYGAPAQDYKKYDVVLLVGLGIGATPMISILKDIINNMKG 764
SIN16   ----LQGENNPNFPRVLIDGPYGAPAQDYKKYEVVLLVGLGIGATPMISIVKDIVNNMKA 760
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SIN18    TVVADAQTEDTRFPKVLIDGPYGAPAQNYKKYDILLLIGLGIGATPFISILKDLLNNIKS 687
SIN20    ----LHGANNPDFPKVLIDGPYGAPAQDYKKYEVVLLVGLGIGATPMISIVKDIVNNIKA 705
SIN22    ----KHWDYIPDFPRILIDGPYGAPAQDYKKFEVVLLVGLGIGATPMISIVSDIINNLKG 735
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                         SEQ ID NO: 32              SEQ ID NO: 33

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SIN2     ------------------------------------------------------------ --
SIN4     MEEEEDASTDLYPPMGRNKPHVDLGTLMTI-TSRPK--KILKTTNAYFYWVTREQGSFDW 824
SIN6     MEEQADLASDFSGNSDMSVATSEQPALNKISLKRRK--STLRTTNAYFYWVTREQGSFDW 843
SIN8     MEEQADLVSDFSGNSDMSAATSEQPALNKISPKKRK--STLKTTNAYFYWVTREQGSFDW 844
SIN10    MEEQADLVSDFSGNSDMSAATSEQPALNKISPKKRK--STLKTTNAYFYWVTREQGSFDW 870
SIN12    MEEHADSISDFSRSSEYSTGSNGD-------TPRRK--RILKTTNAYFYWVTREQGSFDW 825
SIN14    PDRDS-----DIENNNSNNNS-------KG-----------FKTRKAYFYWVTREQGSFEW 802
SIN16    MDEEENSLEDGHNNNMAPNSSPNIAKNKGNKSGSASGGNNFNTRRAYFYWVTREQGSFDW 820
SIN18    NEEVESIHGSEIGSFKNNGPG--------------------RAYFYWVTREQGSFEW 724
SIN20    KEQAQLN--RMENGTSEPQRS-----KKES----------FRTRRAYFYWVTREQGSFDW 748
SIN22    VEEGSNRRQSPIHNMVTPPVSPS---RKSE--------TFRTKRAYFYWVTREQGSFDW 783
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                                                      SEQ ID NO: 34

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SIN2     FKGIMNEIAELDQRNIIEMHNYLTSVYEEGDARSALITMLQALNHAKNGVDVVSXTRVRT 60
SIN4     FKGVMNEIADLDQRNIIEMHNYLTSVYEEGDARSALITMLQALNHAKNGVDIVSGTKVRT 884
SIN6     FKGVMNEVAELDQRGVIEMHNYLTSVYEEGDARSALITMVQALNHAKNGVDIVSGTRVRT 903
SIN8     FKGVMNEVAELDQRGVIEMHNYLTSVYEEGDARSALITMVQALNHAKNGVDIVSGTSVRT 904
SIN10    FKGVMNEVAELDQRGVIEMHNYLTSVYEEGDARSALITMVQALNHAKNGVDIVSGTSVRT 930
SIN12    FKGVMNEVAELDQRGVIEMHNYLTSVYEEGDARSALITMVQALNHAKNGVDIVSGTRVRT 885
SIN14    FKGIMDEISELDEEGIIELHNYCTSVYEEGDARVALIAMLQSLQHAKNGVDVVSGTRVKS 862
SIN16    FKGIMNEAAEMDHKGVIEMHNYCTSVYEEGDARSALITMLQSLHHAKNGVDIVSGTRVKS 880
SIN18    FKGVMNDVAESDHNNIIEMHNYLTSVYEEGDARSALIAMVQSLQHAKNGVDIVSGSRIRT 784
SIN20    FKNIMNEVAERDANRVIEMHNYCTSVYEEGDARSALIHMLQSLNHAKNGVDIVSGTRVMS 808
SIN22    FKNVMDEVTETDRKNVIELHNYCTSVYEEGDARSALITMLQSLNHAKHGVDVVSGTRVMS 843
         **.:*:: :: * . :**:*** ********** *** *:*:*;***:***:** : : :
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SIN2     HFARPNFKRVLSKVAAKHPYAKIGVFYCGAPVLAQELSNLCHEFNGKCTTKF------- 112
SIN4     HFARPNWRKVLSKISSKHPYAKIGVFYCGAPVLAQELSKLCHEFNGKCTTKFEFHKEHF 943
SIN6     HFARPNWKKVFSKTLTKHANARIGVFYCGAPVLAKELSKLCKEYNQKGATKFEFHKEHF 962
SIN8     HFARPNWRKVFSKTLTKHANARIGVFYCGAPILAKELSKLCKEFNQKGTTKFEFHKEHF 963
SIN10    HFARPNWRKVFSKTLTKHANARIGVFYCGAPILAKELSQLCKEFNQKGTTKFEFHKEHF 989
SIN12    HFARPNWKKVLTKLSSKHCNARTGVFYCGVPVLGKELSKLCNTFNQKGSTKFEFHKEHF 944
SIN14    HFAKPNWRQVYKKIAVQHPGKRIGVFYCGMPGMIKELKNLALDFSRKTTTKFDFHKENF 921
SIN16    HFAKPNWRNVYKRIALNHPEAKVGVFYCGAPALTKELRQHALDFSHKTSTKFDFHKENF 939
SIN18    HFARPNWRKVFSDLANAHKNSRIGVFYCGSPTLTKQLKDLSKEFSQTTTTRFHFHKENF 843
SIN20    HFAKPNWRNVYKRIAMDHPNTKVGVFYCGAPALTKELRHLALDFTHKTSTRFSFHKENF 867
SIN22    HFARPNWRSVFKRIAVNHPKTRVGVFYCGAAGLVKELRHLSLDFSHKTSTKFIFHKENF 902
         ***;**:: * . * : ****** . : ::* . . :. . :*:*
```
                           SEQ ID NO: 35

Table summarizing the degree of sequence identity between SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 22. The sequence alignment is performed using CLUSTALW program with the default parameters.

| SEQ ID NO | 2 | 4 | 6 | 8 | 10 | 12 | 14 | 16 | 18 | 20 | 22 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2 | - | - | - | - | - | - | - | - | - | - | - |
| 4 | 89 | - | - | - | - | - | - | - | - | - | - |
| 6 | 79 | 72 | - | - | - | - | - | - | - | - | - |
| 8 | 78 | 72 | 92 | - | - | - | - | - | - | - | - |
| 10 | 78 | 71 | 92 | 98 | - | - | - | - | - | - | - |
| 12 | 76 | 70 | 77 | 77 | 77 | - | - | - | - | - | - |
| 14 | 66 | 52 | 53 | 52 | 52 | 51 | - | - | - | - | - |
| 16 | 66 | 51 | 52 | 51 | 51 | 51 | 67 | - | - | - | - |
| 18 | 64 | 53 | 53 | 53 | 54 | 52 | 49 | 51 | - | - | - |
| 20 | 64 | 50 | 50 | 50 | 50 | 50 | 61 | 65 | 47 | - | - |
| 22 | 62 | 52 | 52 | 52 | 51 | 51 | 59 | 60 | 50 | 62 | - |